

Amendments to the Specification:

Please replace paragraph [49] beginning at page 12, line 32, with the following:

--[49] In some embodiments, the reaction mixtures further comprise a detectably-labeled oligonucleotide that hybridizes to SEQ ID NO:25 or a complement thereof. In some embodiments, the reaction mixtures further comprise a detectably-labeled oligonucleotide comprising FGGTCTAGAIGGTTAGAGGAGACCCTCCAG (SEQ ID NO:75), wherein F is CY5[[:]] and I is FAM; P is PO4; U is propynyl dU; and E is 5-methyl dC. In some embodiments, the reaction mixtures further comprise a detectably-labeled oligonucleotide that hybridizes to SEQ ID NO:16 or a complement thereof.--

Please replace paragraph [53] beginning at page 13, line 22, with the following:

--[53] In some embodiments, the detectably-labeled oligonucleotide comprises FGGTCTAGAIGGTTAGAGGAGACCCTCCAG (SEQ ID NO:75), wherein F is CY5 and I is FAM. In some embodiments, the detecting step comprises hybridizing a detectably-labeled oligonucleotide that hybridizes to SEQ ID NO:16, or a complement thereof, to the amplified nucleic acid of the nucleic acid of yellow fever virus; and detecting hybridization of the detectably-labeled oligonucleotide to the amplified nucleic acid.--

Please replace paragraph [58] beginning at page 14, line 16, with the following:

--[58] In some embodiments, the kits further comprise a detectably-labeled oligonucleotide that hybridizes to SEQ ID NO:16 or a complement thereof. In some embodiments, the kits further comprise a detectably-labeled oligonucleotide that hybridizes to

SEQ ID NO:25 or a complement thereof. In some embodiments, the kits further comprise a detectably-labeled oligonucleotide comprising
FGGTCTAGAIGGTTAGAGGAGACCCTCCAG (SEQ ID NO:75), wherein F is CY5 and I is FAM.--

Please replace paragraph [70] (as amended) beginning at page 16, line 29, with the following:

--[70] Figure 1 presents a region of conserved sequence, identified as SEQ ID NO.: 1, in the 3' untranslated region of the genomes of the flaviviruses that can be detected using the compositions and methods of the present invention and that can be bound by a primer of the invention. SEQ ID NO.: 2 represents the complement of SEQ ID NO.: 1. ~~Flavivirus AF196835 = SEQ ID NO:71.~~ The conserved region in the 3' untranslated region of the genomes of the flaviviruses = SEQ ID NOS:71 and 81-241, respectively.--

Please replace paragraph [71] (as amended) beginning at page 16, line 33, with the following:

--[71] Figure 2 presents a region of conserved sequence, identified as SEQ ID NO.: 9, in the 3' untranslated region of the genomes of the flaviviruses that can be detected using the compositions and methods of the present invention and that can be bound by a primer of the invention. SEQ ID NO.: 10 represents the complement of SEQ ID NO.: 9. ~~Flavivirus AF196835 = SEQ ID NO:72.~~ The conserved region in the 3' untranslated region of the genomes of the flaviviruses = SEQ ID NOS:72 and 242-315, respectively.--

Please replace paragraph [72] (as amended) beginning at page 17, line 3, with the following:

--[72] Figure 3 presents a region of conserved sequence, identified as SEQ ID NO.: 16, in the 3' untranslated region of the genomes of the flaviviruses that can be detected

using the compositions and methods of the present invention and that can be bound by a probe of the invention. SEQ ID NO.: 17 represents the complement of SEQ ID NO.: 16. ~~Flavivirus AF196835 = SEQ ID NO:73.~~ The conserved region in the 3' untranslated region of the genomes of the flaviviruses = SEQ ID NO:73 and 316-605, respectively.--

Please replace paragraph [73] (as amended) beginning at page 17, line 7, with the following:

--[73] Figure 4 presents an alignment of the nucleic acid sequences (~~SEQ ID NOS:7, 15 and 16~~) of the oligonucleotides of the invention with nucleic acid sequences of Japanese encephalitis virus serogroup members (SEQ ID NOS:7, 606-670, 7, 671-736, 15, 737-788, 16 and 789-839, respectively).--

Please replace paragraph [74] (as amended) beginning at page 17, line 10, with the following:

--[74] Figure 5 presents an alignment of the nucleic acid sequences (~~SEQ ID NO:16~~) of the oligonucleotides of the invention with nucleic acid sequences of detectable flaviviruses that are not members of the Japanese encephalitis virus serogroup (SEQ ID NOS:16, 840-909, 16 and 910-919, respectively).--

Please replace paragraph [112] beginning at page 28, line 3, with the following:

--[112] In certain embodiments, the first nucleic acid primer comprises at least about 16 consecutive nucleotides of SEQ ID NO.: 2. ~~SEQ ID NO.: 2, as shown in Figure 1,~~ is the complement to SEQ ID NO.: 1, ~~as shown in Figure 1.~~ In other embodiments, the first nucleic acid primer comprises at least about 18 consecutive nucleotides of SEQ ID NO.: 2. In still other embodiments, the first nucleic acid primer comprises at least about 20 consecutive nucleotides of SEQ ID NO.: 2. In yet other embodiments, the first nucleic acid primer comprises at least about

22 consecutive nucleotides of SEQ ID NO.: 2. In still other embodiments, the first nucleic acid primer comprises at least about 24 consecutive nucleotides of SEQ ID NO.: 2.--

Please replace paragraph [119] beginning at page 31, line 15, with the following:

--[119] In certain embodiments, the second nucleic acid primer comprises at least 16 consecutive nucleotides of SEQ ID NO.: 10. ~~As shown in Figure 2,~~ SEQ ID NO.: 10 represents the complement of SEQ ID NO.: 9, as shown in Figure 2. In other embodiments, the second nucleic acid primer comprises at least about 18 consecutive nucleotides of SEQ ID NO.: 10. In still other embodiments, the second nucleic acid primer comprises at least about 20 consecutive nucleotides of SEQ ID NO.: 10. In yet other embodiments, the second nucleic acid primer comprises at least about 22 consecutive nucleotides of SEQ ID NO.: 10. In still other embodiments, the second nucleic acid primer comprises at least about 24 consecutive nucleotides of SEQ ID NO.: 10.--

Please replace paragraph [163] beginning at page 46, line 11, with the following:

--[163] In some embodiments, the following probe variants are used:
FGGACTAGAIGGTTAGAGGAGACCCCGCGGP (SEQ ID NO:76, which is a variant of SEQ ID NO:28);
FGGAEUAGAIGGUUAGAGGAGAEEEEGEGGP (SEQ ID NO:77, which is a variant of SEQ ID NO:28);
FGGGTCTCCITCTAACCTCTAGTCCTTCCCCCP (SEQ ID NO:78, which is a variant of SEQ ID NO:70);
FGGGUEUEEIEUAACCTCTAGTCCTTCCCCCP (SEQ ID NO:79, which is a variant of SEQ ID NO:70); and
FGGTCTAGAIGGTTAGAGGAGACCCTCCAGP (SEQ ID NO:80, which is a variant of SEQ

Appl. No. 10/815,480
Amdt. dated August 22, 2008
Reply to Office Action of June 23, 2008

PATENT

ID NO:25). In all of the above probes, F = CY5; I = FAM; P = PO4; U = propynyl dU; E = 5-methyl-dC).--

Please cancel the present "SEQUENCE LISTING", pages 1-21, submitted July 15, 2004, and insert therefor the accompanying paper copy of the Substitute Sequence Listing, page numbers 1 to , at the end of the application.